

## BEST AVAILABLE COPY

INFORMATION FOR SEQ ID NO: 109:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1524 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-020-956-109

Alignment Scores:  
Pred. No.: 8,44e-287 Length: 1524  
Score: 320.00 Matches: 320  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 28.4% Indels: 0  
DB: 3 Gaps: 0

US-10-643-795a-123 (1-1127) x US-09-020-956-109 (1-1524)

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QY 766 LeuArgGInGlyLeuSerGlyGlySerLeuAlaSerGlyProGlyProGly 785
DB 10 CTGCGCCAGGGGCTGAGCGGAGCGGGGCGAGCTCGCCAGCGGGGCGCCCGGCTGAG 69
QY 786 HisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAngInCysAsp 805
DB 70 CATGCTCTACATGAGCGAGCGGCTGCGCTTACTCTGCGGACAGCTGGAACAGATGCGAC 129
QY 806 LeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeuTyr 825
DB 130 CTAGGGGCTCTACCGCTTCTTCCCTGGGGGCTGGCGGTGCGGCTGACCCCGGGTTTGTC 189
QY 826 HisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuHis 845
DB 190 CACCTGGGGCGGACCTGCTCTGTCATCGACTTCATGATGTTTTCACGCGTGGCTCTTAC 249
QY 846 IlePheThrValAsnLysGlnLeuGlyProLysIleValIleValSerLysMetLys 865
DB 250 ATCTTCACGCTCAACAAAGCTGGGGGCCCAAGATGTCATGTCAGCAAGATGATGATG 309
QY 866 AspValPhePhePheLeuPhePheLeuGlyValITrPLeuValAlaTyrGlyValAlaThr 885
DB 310 GACGAGTCTCTTCTCTTCTTCTTCTGCGGCGTGGCTGAGCTATGCGGTGGCGAG 369
QY 886 GlnGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPheTyr 905
DB 370 GAGGGGCTCTGAGGGCGAGGACAGTGACTTCCCAAGTATCTTGGCGCGCTTCTTAC 429
QY 906 ArgProTyrLeuGlnIlePheGlyGlnIleProGlnLysAspMetAspValAlaLeuMet 925
DB 430 CTTCTCTTCTGACATCTTCTGGGACGATTTCCCAAGAGACATGACCTGGCTCTCAG 489
QY 926 GlnHisSerAsnCysSerSerGlnProGlyPheTrpAlaHisProProGlyValAlaGlnAla 945
DB 490 GAGCAGCAGCACTGCTCGTGGAGCGCGGCTTCTGGGACACCTCTCTGGGGCCAGGG 549
QY 946 GlyThrCysValSerGlnTyrAlaAsnTrpLeuValValLeuLeuValIlePheLeu 965
DB 550 GGCACCTGGGTCTCCCAAGTATGCCAATGCTGGGTGCTCTCTCTCTCATCTTCTCG 609
QY 966 LeuValAlaAsnIleLeuLeuValAlaLeuLeuIleAlaMetPheSerTyrThrPheGly 985
DB 610 CTCTGGGCCAATCTCTGCTGTCATCTGCTCATTTGCCATGTCAGTTACATTCAGC 669
QY 986 LysValGlnGlyAsnSerAspLeuTyrTrpValAlaGlnArgTyrArgLeuIleArgGln 1005
DB 670 AAAGTACAGGGGCAACGAGATCTCTATGAAAGGCGCAGCGTATCCGCTCTCCGGAA 729
QY 1006 PheHisSerArgProAlaLeuAlaProPheIleValIleSerHisLeuArgLeu 1025
DB 730 TTCACATCTGGCCCGCGCTGGCCCGCTTATATGTCATCTCCCATTTGGGCTCTCTG 789
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QY 1026 LeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlnHis 1045
DB 790 CTGAGCATTTGTGAGGCGAGCCCGGAGCCCGGCTCTCTCCCGGCTCTGAGCAT 849
QY 1046 PheArgValTyrLeuSerLysGlnAlaGlnArgLysLeuLeuThrTrpGlnSerValHis 1065
DB 850 TTCCGGGTTTACTTTCTTCAAGAAAGCCGAGCGGAAGCTGCTTACCTGGGAATCGGTGCAT 909
QY 1066 LysGlnAsnPheLeuLeuValAlaArgAlaArgAspLysArgGlnSerAspSerGlnArgLeu 1085
DB 910 AAGGAACCTTCTGCTGCGACGCGCTAGGACAAAGCGGAGAGCTCTCGAGGCTCTG 969
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## RESULTS

US-09-020-956-109 (1-1524)  
Sequence alignment with US-10-643-795a-123 (1-1127)  
Percent: 62.62215

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FC  
NUMBER OF SEQUENCES: 224

## CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98104

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,607

## CLASSIFICATION:

FILING DATE: 25-FEB-1998

## ATTORNEY/AGENT INFORMATION:

NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392

TELEPHONE/DOCKET NUMBER: 210121.427C3

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

## INFORMATION FOR SEQ ID NO: 109:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1524 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-030-607-109

## ALIGNMENT SCORES:

Pred. No.: 8,44e-287 Length: 1524  
Score: 320.00 Matches: 320  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 28.4% Indels: 0  
DB: 3 Gaps: 0

US-10-643-795a-123 (1-1127) x US-09-030-607-109 (1-1524)

```
QY 766 LeuArgGInGlyLeuSerGlyGlySerLeuAlaSerGlyProGlyProGly 785
DB 10 CTGCGCCAGGGGCTGAGCGGAGCGGGGCGAGCTCGCCAGCGGGGCGCCCGGCTGAG 69
QY 786 HisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAngInCysAsp 805
DB 70 CATGCTCTACATGAGCGAGCGGCTGCGCTTACTCTGCGGACAGCTGGAACAGATGCGAC 129
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Exhibit A

Qy	806	LeuValAlaLeuThrCysPheLeuLeuGlyValGlyArgLeuThrProGlyLeu	825
Db	130	CTAGGAGCTTCACCTGCTCTCTCTGAGCGGAGCTGCGGCTAACCCCGGATTGTAC	189
Qy	826	HisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeuHis	845
Db	190	CACCTGGGCGCCGACCTGCTCTCTGCATCGACTTCATCGTTTCAACGGTGGCGCTGCTTAC	249
Qy	846	IlePheThrValAsnIleGlnLeuGlyProValIleValIleValSerIleMetMetLeys	865
Db	250	ATCTTCACGGCTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTAGCAAGATGATGAAG	309
Qy	866	AspValPhePhePheLeuPhePheLeuGlyValITripLeuValAlaTyrGlyValAlaThr	885
Db	310	GACGGTTCCTCTTCTCTCTCTCTCTGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	369
Qy	886	GluGlyLeuLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPheTyr	905
Db	370	GAGGGAGCTTCCTGAGGCGACGGGACAGTGAATTCCTCCAAAGTATCTTGCGCGGCTTCTTAC	429
Qy	906	ArgProTyrLeuGlnIlePheGlyGlnIleProGlnGluAspMetAspValAlaLeuMet	925
Db	430	CGTCCCTACCTGCAATCTCTGGGAGAGANTCCCGAGAGGACATGGAGCTGGCCCTCATG	489
Qy	926	GluHisSerAsnCysSerSerGluProGlyPheTTPAlaHisProProGlyValAlaGlnAla	945
Db	490	GAGGACACACACTGCTCTGCGGAGCCCGGCTTCTTGAGGCACACCTCTCTGGGCGCCAGGGG	549
Qy	946	GlyThrCysValSerGlnTyrValAlaMetPheLeuValValLeuLeuLeuValIlePheLeu	965
Db	550	GGCACCTGGCTCTCCAGATGCAACACTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG	609
Qy	966	LeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyrThrPheGly	985
Db	610	CTCGGCGCCACATCTCTGTGTCTCAACTTGCTCATTTGCCATGTTCACTTACATTCGCG	669
Qy	986	LysValGlnGlyAsnSerAspLeuTyrTyrValGlnArgTyrArgLeuIleArgGln	1005
Db	670	AAAGTACAGGGCAACAGCATCTTACTGGAAGGCGCAACGTTACCGCTCATCCGGGAA	729
Qy	1006	PheHisSerArgProAlaLeuAlaProPheIleValIleSerHisLeuArgLeuLeu	1022
Db	730	TTCCACTCTCGGCGCGCGCTGGCCCGCCCTTATCGTATCTCCCATCTGGCGCTCTCG	789
Qy	1026	LeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlnHis	1044
Db	790	CTCAGGCATTTGACGAGGACCCCGGAGCCCGCCACCGCTCTCTCCCGGCTCTCGAGCAT	849
Qy	1046	PheArgValTyrLeuSerIleGlyGlnArgIleGlyLeuThrTyrGluSerValHis	1065
Db	850	TTCCGGGTTTACTTCTTCTAAGGAAGCCGAGCGGAACCTCTAACGAGGGAATCGTGAT	909
Qy	1066	LysGluAsnPheLeuLeuAlaArgAlaArgAspLysArgGluSerAspSerGluArgLeu	1088
Db	910	AAGGAGAACTTTCTGCTGGCAGCGCTAGGAGCAACGCGGAGAGCGATCCGAGCGTCTG	969

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; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-109

Alignment Scores:
Pred. No.:      8,44e-287      Length:      1,524
Score:          320.00        Matches:      320
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatch:         0
Query Match:     28.4%       Indels:          0
DB:              3           Gaps:            0

US-10-643-795A-123 (1-1127) x US-09-439-313-109 (1-1524)
QY      766  LeuArgGInGlyLeuSerGIyGIyGIySerLeuAlaSerGIyGIyProGIyProGIy      785
DB      10  CTGGCCCAAGGGCTGAGGCGAGAGCGGGGGCAGCTTCGCCAGGGGGGGCCCCGGGCTGGC    69
QY      786  HisAlaSerLeuSerGIyAlaArgLeuArgLeuYyLeuAlaAspSerTrpAngInGyAsp    805
DB      70  CATGGCTCAGTCAGGCACAGCGCTGGGCTCTTACCTCGCCGACAGCTGGAACAGATGCGAC    129
QY      806  LeuValAlaLeuThrCyAsPheLeuLeuGIyValGIyCyAsArgLeuThrProGIyLeuTyR    825
DB      130  CTAGGGGCTCTTCACCTGCTCTTCCTCGGGCGGGGCTGCCGCTACCCCCGGGTTGTGAC    189
QY      826  HisLeuGIyArgThrValLeuCyAsIleAspPheMetValPheThrValArgLeuLeuHis    845
DB      130  CACCTGGGGCGGACTGCTCTCTGCACTCACTTCAAGTTTACAGGTCGGCTGCTTCAAC    249
QY      846  IlePheThrValAsnIleGlnLeuGIyProIyIleValIleValSerIyMetMetIys    865
DB      250  ATCTTCACAGGTCAACAACAGCTGGGGGCCCAAGATCGTATCGTGAAGCAATGATGAAG    309
QY      866  AspValPhePhePheLeuPhePheLeuGIyValITrPLeuValAlaTyGIyValAlaThr    885
DB      310  GACGGGTCTTCTTCTCTCTCTCTCTCGCGCGTGGCTGTGTGCTATGGCGTGGCGACG    369
QY      886  GInGlyLeuLeuAsyProArgAspSerAspPheProSerIleLeuArgArgValPheTyR    905
DB      370  GAGGGGGCTCTCGAGGGCCACGGGAGCAGTACTTCCCAAGATCTTGGCGCGGCTTCTAC    429
QY      906  ArgProTyRLeuGInIlePheGIyGInIleProGInGInIAspMetAspValAlaLeuMet    925
DB      430  CGTCCCTTACCTGCAGATCTTCGGGAGATTCGCCAGAGACATGGAAGCTGGCCCTCAG    489
QY      926  GInHisSerAsnCySerSerSerGIuProGIyPheITrPalHisProProGIyValaGInAla    945
DB      490  GAGCACAAGCAACTGCTCGTCGAGGCCCGGCTTCTGGGCAACCTCTCGGGGCCCAAGGCG    549
QY      946  GInTyRValSerGIuTrpAlaAsnTrpLeuValValIleLeuLeuValIlePheLeu    965
DB      550  GGCACCTCGCTTCCAGATGCAACCACTGAGCTGGTGAGTGCTCTCTGTCATCTTCTCG    609
QY      966  LeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyRThrPheGIy    985
DB      610  CTCGGGGCCACATCTCTGCTGTCACCTTGCATTCGCATTCGCATTCGATTCACATTCGGC    669
QY      986  IysValGIyGIyAsnSerAspLeuTyRTrpIyValaGInaGTYArgLeuIleArgGIn    1005
DB      670  AAAGTACAGGGCAACAGCATCTTACATGGAAGCGCAGCGCTTACCGGCTCATCCGGGA    729
QY      1006  PheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgLeuLeu    1025
DB      730  TTCACCTCTCGGCTCGGCTGGCCCCGGCCCTTATGTCATCTCCCACTTGGCTTCTCG    789

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PR 06-APR-2001; 2001US-0281922P.  
 PR 24-APR-2001; 2001US-0286214P.  
 PR 30-APR-2001; 2001US-00847046.  
 PR 04-MAY-2001; 2001US-0285859P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P,  
 DR MPI; 2002-471335/50.  
 P-PSDB; AB61852.  
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,  
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,  
 PT by determining if prostate cancer-associated genes are expressed in a  
 PT prostate tissue.  
 PS Claim 22; Page 339-340; 436pp; English.  
 XX  
 CC The present invention relates to methods of detecting a prostate cancer-  
 CC associated transcript in a cell from a patient. The method comprises  
 CC contacting a biological sample from the patient with prostate cancer-  
 CC associated polynucleotides (designated PC genes) that selectively  
 CC hybridize to a sequence that is at least 80% identical to them. The  
 CC expressed in prostate tumour tissue or in prostate cancer and are derived  
 CC from the tissues of various organisms such as humans or other mammals  
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
 CC associated genes are useful for diagnosing or treating prostate cancer,  
 CC as well as for identifying modulators of prostate cancer or agents that  
 CC inhibit prostate cancer. The nucleic acid sequences are particularly  
 CC useful in gene therapy, as a vaccine or in antisense applications.  
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide  
 CC sequences  
 XX  
 SO Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 3810  
 Score: 1123.00 Matches: 1123  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 59.6% Indels: 0  
 DB: Gaps: 0  
 US-10-643-795A-123 (1-1127) x ABK92167 (1-3810)  
 QY 5 ThrGtulyPrpThrAAspAlaTyrGlyLeuAAspPheThrGlyAlaGlyAArgHis 24  
 DB 3 ACGGGAAGCCCAAGATGCTTACGAGAGCTGACCTTCAAGGGGCGCGCGCAAGAC 62  
 QY 25 SerAenPheLeuArgLeuSerAspArgThrAAspProAlaAlaValTyrSerLeuValThr 44  
 DB 63 AGCATTTCTCCGCTCTCTGACCGAAGGATCCAGCTGAGTTTATPAGTGTGCTACA 122  
 QY 45 ArgThrTrpGlyPheArgAlaProAlaLeuValSerValLeuGlyGlySerGlyGly 64  
 DB 123 CGCAGATGGGGCTTCGTCCTCCGGAACCTGGTGCTGCTGCTGGGGGAGTGGGGGGC 182  
 QY 65 ProValLeuGlnThrTrpLeuGlnAspLeuLeuAAspArgGlyLeuValArgAlaAlaGln 84  
 DB 183 CCGGCTCTCAAGACCTGGCTGAGAGCTGCTGCTGCTGCTGGGCTGGTGGCGCTGCCAG 242  
 QY 85 SerThrGlyAlaTrpIleValThrGlyGlyLeuHisThrGlyIleGlyAArgHisValGly 104  
 DB 243 AGCAGCAGGAGCCCGATTTGCTGCTGGGGGTCTGCAACGGGCGATCGCGCGCATGTGGT 302  
 QY 105 ValAlaValArgAspHisGlnMetAlaSerThrGlyGlyThrIleValAlaMetGly 124  
 DB 303 GTGGCTGTACGGGACCATGATGGCCAGACCTGGGGGCGCAAGGTGGTGGCCATGGGT 362  
 QY 125 ValAlaProTrpGlyValValArgAsnArgAspThrLeuIleAsnProIleGlySerPhe 144

DB 363 GTGGCCCCCTGGGGGTGTGCTCCGAAATGAGACACCTTCATCAACCCCAAGGGCTCGTTCC 422  
 QY 145 ProAlaArgTyrArgTrpArgGlyAAspProGluAAspGlyValGlnPheProLeuAspTyr 164  
 DB 423 CTGGCAGAGTACCGGTGGCGGTGACCCGAGAGAGCGGGGTCAAGTTTCCCTGAGACTAC 482  
 QY 165 AsnTyrSerAlaPhePheLeuValAspAspGlyThrHisGlyCysLeuGlnGlyGlnAsn 184  
 DB 483 AACTACTGGGCTTCTCTCTGCTGAGACACCGACACACGGCTGCTGGGGGCGAGAAC 542  
 QY 185 ArgPheArgLeuArgLeuGlnSerTyrIleSerGlnGlnIleThrGlyValGlyGlyThr 204  
 DB 543 CCGTTCGGCTGGCTGGAGTCTTCACTTCAACAGACAGACCGGGCTGGGGAGGACT 602  
 QY 205 GlyIleAspIleProValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 224  
 DB 603 GGAATTGACATCCCT 662  
 QY 225 IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyGlyAla 244  
 DB 663 ATAGAGAACGCCACCGAGCTCAGCTCCCATGTCTCTCTCTCTCTCTCTCTCTCTCTCT 722  
 QY 245 AlaAspCysLeuAlaGlnThrLeuGluAAspThrLeuAlaProGlySerGlyGlyAlaArg 264  
 DB 723 GCGGACTGCTGGCGGAGACCTCGAAGACACTTGGCCCGAGGAGTGGGGAGCCAGG 782  
 QY 265 GlnGlyGlnAlaArgAspArgIleArgArgPhePheProIleGlyAAspLeuValLeu 284  
 DB 783 CAGGGCGAAGCCCGAATGATGATCAGAGCTTCTTCCAAAGGGAGCTTGGAGCTCTG 842  
 QY 285 GlnAlaGlnValGlnArgIleMetThrArgGlyGlnLeuLeuThrValTyrSerSerGln 304  
 DB 843 CAGGGCCAGGTGAGAGATTAAGACCCCGAAGAGCTCTTGAACGTATTTCTTGAG 902  
 QY 305 AspGlySerGlnGlnPheGlnThrIleValLeuValAlaLeuValValCysGlySer 324  
 DB 903 GATGGGCTGAGGAATTCGAGACCATGATTTTGAAGGCTTGTGAAGGCTGTGGAGC 962  
 QY 325 SerGlnAlaSerAlaTyrLeuAAspGluLeuArgLeuAlaValAlaTrpAsnArgValAsp 344  
 DB 963 TCGGAGGCTCAGGCTACCTGATGAGCTGCTGTGGCTGTGGCTGGAACCGGTGAGC 1022  
 QY 345 IleAlaGlnSerGlnLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla 364  
 DB 1023 ATTGCCAGAGTGAATCTTTCGGGGGAGACATCCATGCGGCTCTTCACTTGAAGCT 1082  
 QY 365 SerLeuMetAspAlaLeuLeuAAspArgProGluPheValArgLeuLeuLeuSerHis 384  
 DB 1083 TCCTCTCATGACGCTCTGATGATGACCGGCTGATGCTGCGCTGCTCATTTCCAC 1142  
 QY 385 GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaAla 404  
 DB 1143 GGCTTCAAGCTGGGCGCACTTCTGACCCCGATGCGCTGGGCCCACTTCAAGCGCGCGC 1202  
 QY 405 ProSerAsnSerLeuIleArgAsnLeuLeuAspGlnAlaSerHisSerAlaGlyThrHis 424  
 DB 1203 CCTTCAACTGCTCATCTCCGACACCTTTTGGACCAAGGGGTCCACAGGGCGAGCACTAA 1262  
 QY 425 AlaProAlaLeuValGlyValAlaAlaGlnLeuArgProProAspValGlyHisValLeu 444  
 DB 1263 GCCCAGGCTTAAAGGGGAGAGCTGGAGGCTTCCGCGCCCTGAGCGTGGGAGATGGCTG 1322  
 QY 445 ArgMetLeuLeuGlyIleMetCysAlaProArgTyrProSerGlyGlyAlaTrpAspPro 464  
 DB 1323 AGGATGCTGCTGGGGAATATGCGCGCGAGATACCCCTCGGGGGGCGCTGGAGACCT 1382  
 QY 465 HisProGlyGlnGlyPheGlyGlnSerMetTyrLeuLeuSerAspValAlaThrSerPro 484  
 DB 1383 CACCCAGGCGCAGGGGCTTGGGGAGAGCATGTATGCTCTTGAACAGGCCACTTCCCGC 1442  
 QY 485 LeuSerLeuAspAlaGlyLeuGlyGlnAlaProTrpSerAspLeuLeuLeuTrpAlaLeu 504



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